

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/721,047
Source: IFWO
Date Processed by STIC: 03/15/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/721,047</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	<u>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)</u>	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING

DATE: 03/15/2006

PATENT APPLICATION: US/10/721,047

TIME: 11:27:14

Input Set : A:\020444-000110US.ST25.txt

Output Set: N:\CRF4\03152006\J721047.raw

3 <110> APPLICANT: Target Discovery, Inc.

4 Schneider, Luke V.

5 Peterson, Jeffery N.

6 Hall, Michael P.

7 Petesch, Robert

9 <120> TITLE OF INVENTION: Polypeptide Fingerprinting Methods and Bioinformatics

Database System

11 <130> FILE REFERENCE: 020444-000110US

13 <140> CURRENT APPLICATION NUMBER: US 10/721,047

14 <141> CURRENT FILING DATE: 2003-11-21

16 <150> PRIOR APPLICATION NUMBER: US 09/513,907

17 <151> PRIOR FILING DATE: 2000-02-25

19 <150> PRIOR APPLICATION NUMBER: US 60/130,238

20 <151> PRIOR FILING DATE: 1999-04-20

22 <160> NUMBER OF SEQ ID NOS: 5

24 <170> SOFTWARE: PatentIn version 3.1

26 <210> SEQ ID NO: 1

27 <211> LENGTH: 12

28 <212> TYPE: PRT

29 <213> ORGANISM: 1425.7 Da peptide

31 <400> SEQUENCE: 1

33 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg

34 1 5 10

37 <210> SEQ ID NO: 2

38 <211> LENGTH: 6

39 <212> TYPE: PRT

40 <213> ORGANISM: Glycogen Phosphorylase

42 <400> SEQUENCE: 2

44 Ser Arg Pro Leu Ser Asp

45 1 5

48 <210> SEQ ID NO: 3

49 <211> LENGTH: 4

50 <212> TYPE: PRT

51 <213> ORGANISM: Bradykinin

53 <400> SEQUENCE: 3

55 Arg Pro Pro Gly

56 1

59 <210> SEQ ID NO: 4

60 <211> LENGTH: 5

61 <212> TYPE: PRT

62 <213> ORGANISM: Bradykinin

64 <400> SEQUENCE: 4

66 Arg Pro Pro Gly Phe

67 1 5

Does Not Comply
Corrected Diskette Needed

Cp9-1,27

Invalid Response. (213) Response
Can be either Artificial,
Unknown or Genus Species.
See Item 10 on
Error Summary sheet.

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Input Set : A:\020444-000110US.ST25.txt

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70 <210> SEQ ID NO: 5

71 <211> LENGTH: 6

72 <212> TYPE: PRT

73 <213> ORGANISM: Bradykinin *same error*

75 <400> SEQUENCE: 5

77 Arg Pro Pro Gly Phe Ser

78 1 5

VERIFICATION SUMMARY

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